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Conference Abstract

Linking molecular and morphological biodiversity evidence by building a single name space

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Abstract

GBIF is working on the solution to represent molecular (DNA) evidence of species presence in time and space alongside the currently prevailing morphological evidence. Among many benefits of this approach are filling the geographic and taxonomic gaps and adequate representation of functionally important organism groups. Experimental modification of GBIF backbone includes provisional non-Linnaean names from UNITE and BOLD systems, enabling indexing georeferenced sequences alongside other records. Life on Earth does not depend on the language we use to name taxa, single index and access point to global biodiversity data is essential for good science and adequate decision making.

Keywords

GBIF, backbone, OTU, nomenclature

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